

SEQUENCE LISTING

5

(1) GENERAL INFORMATION:

- (i) APPLICANT: Sato, Takaaki
- 10 (ii) TITLE OF INVENTION: TREX, A NOVEL GENE OF TRAF-INTERACTING
EXT GENE FAMILY AND DIAGNOSTIC AND THERAPEUTIC USES
THEREOF
- (iii) NUMBER OF SEQUENCES: 37
- 15 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Cooper & Dunham LLP
(B) STREET: 1185 Avenue of the Americas
(C) CITY: New York
20 (D) STATE: New York
(E) COUNTRY: U.S.A
(F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
25 (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- 30 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- 35 (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: White, John P.
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 0575/51902-A-PCT
- 40 (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 278-0400
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45 (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3479 base pairs
(B) TYPE: nucleic acid
50 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- 55 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 458..3211
- 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	CTGATCGTT	GGTAGTGGCA	TGGAGGACGG	GGCTGGCATT	TCAGACTGCC	AGCTGTTTTT		60										
	ACCAGCCGCT	GCATCACTTG	AATAGAAGCT	ATGCATATTG	GCTGGCCGAC	AAAGCCAAGG		120										
	5GACAAAAGCT	ATGGCCGTTA	AAATGGTCCC	TCTGAGTCCA	GGGCTCTTTC	CCTGGCTTTT		180										
	AGCACCATGG	ATCTCTTCTT	TTTCATCCCA	TCAGCAATGT	GGTACCTTCT	TCTACTTGAT		240										
	GATGACAGCT	GATACTTCAG	ATTTCGCTGA	CTAAGGTTAG	AAACCTGAAT	CGCTGTGAGG		300										
10	AAGATGAAAT	TTCCATTTTA	CTTGGTGCCT	TGTGCAGGGA	GCACACTGAT	CCTTCCAGAA		360										
	ACTTGTGTGT	AAAAAGAGGT	TGCGTTTTGT	CAGACAGACT	CATGTTTATG	GCAGAGCGATC		420										
15	CGACGTGATC	AGAGTGGGCA	AGAGGCACAG	CGAACTC	ATG	ACA	GGC	TAT	ACC	ATG		475						
				Met	Thr	Gly	Tyr	Thr	Met									
				1				5										
	TTG	CGG	AAT	GGG	GGA	GTG	GGG	AAC	GGT	GGT	CAG	ACC	TGT	ATG	CTG	CGC		523
20	Leu	Arg	Asn	Gly	Gly	Val	Gly	Asn	Gly	Gly	Gln	Thr	Cys	Met	Leu	Arg		
				10					15					20				
	TGG	TCC	AAT	CGC	ATC	CGG	CTG	ACA	TGG	CTG	AGT	TTC	ACG	CTG	TTC	ATC		571
25	Trp	Ser	Asn	Arg	Ile	Arg	Leu	Thr	Trp	Leu	Ser	Phe	Thr	Leu	Phe	Ile		
			25					30					35					
	ATC	CTC	GTC	TTC	TTC	CCC	CTC	ATT	GCT	CAC	TAT	TAC	CTC	ACC	ACT	CTG		619
30	Ile	Leu	Val	Phe	Phe	Pro	Leu	Ile	Ala	His	Tyr	Tyr	Leu	Thr	Thr	Leu		
			40				45					50						
	GAC	GAG	GCA	GAC	GAG	GCT	GGC	AAG	CGC	ATC	TTC	GGC	CCT	CGG	GCT	GGC		667
	Asp	Glu	Ala	Asp	Glu	Ala	Gly	Lys	Arg	Ile	Phe	Gly	Pro	Arg	Ala	Gly		
	55					60					65					70		
35	AGT	GAG	CTC	TGT	GAG	GTA	AAG	CAT	GTC	CTT	GAT	CTC	TGT	CGG	ATT	CGT		715
	Ser	Glu	Leu	Cys	Glu	Val	Lys	His	Val	Leu	Asp	Leu	Cys	Arg	Ile	Arg		
					75					80					85			
	GAG	TCT	GTG	AGC	GAA	GAG	CTT	CTA	CAG	CTC	GAA	GCC	AAG	CGG	CAG	GAG		763
40	Glu	Ser	Val	Ser	Glu	Glu	Leu	Leu	Gln	Leu	Glu	Ala	Lys	Arg	Gln	Glu		
				90					95					100				
	CTG	AAC	AGC	GAG	ATT	GCC	AAG	CTG	AAC	CTC	AAG	ATT	GAA	GCC	TGT	AAG		811
45	Leu	Asn	Ser	Glu	Ile	Ala	Lys	Leu	Asn	Leu	Lys	Ile	Glu	Ala	Cys	Lys		
			105					110				115						
	AAG	AGC	ATA	GAG	AAT	GCC	AAG	CAG	GAC	CTG	CTG	CAG	CTC	AAG	AAT	GTC		859
50	Lys	Ser	Ile	Glu	Asn	Ala	Lys	Gln	Asp	Leu	Leu	Gln	Leu	Lys	Asn	Val		
		120					125					130						
	ATT	AGC	CAG	ACA	GAG	CAC	TCC	TAC	AAG	GAG	CTG	ATG	GCC	CAG	AAC	CAG		907
	Ile	Ser	Gln	Thr	Glu	His	Ser	Tyr	Lys	Glu	Leu	Met	Ala	Gln	Asn	Gln		
	135					140					145					150		
55	CCC	AAA	CTG	TCC	CTG	CCC	ATC	CGA	CTG	CTC	CCT	GAG	AAG	GAC	GAT	GCC		955
	Pro	Lys	Leu	Ser	Leu	Pro	Ile	Arg	Leu	Leu	Pro	Glu	Lys	Asp	Asp	Ala		
					155					160					165			
	GGC	CTT	CCA	CCC	CCC	AAG	GTC	ACT	CGG	GGT	TGC	CGC	CTT	CAC	AAC	TGC		1003
60	Gly	Leu	Pro	Pro	Pro	Lys	Val	Thr	Arg	Gly	Cys	Arg	Leu	His	Asn	Cys		
				170					175					180				
	TTT	GAT	TAC	TCT	CGT	TGT	CCT	CTG	ACG	TCT	GGC	TTT	CCC	GTC	TAC	GTC		1051

	Phe	Asp	Tyr	Ser	Arg	Cys	Pro	Leu	Thr	Ser	Gly	Phe	Pro	Val	Tyr	Val	
			185					190					195				
	TAT	GAC	AGT	GAC	CAG	TTT	GCC	TTT	GGG	AGC	TAC	CTG	GAC	CCT	TTG	GTC	1099
5	Tyr	Asp	Ser	Asp	Gln	Phe	Ala	Phe	Gly	Ser	Tyr	Leu	Asp	Pro	Leu	Val	
		200					205					210					
	AAG	CAG	GCT	TTT	CAG	GCT	ACA	GTG	AGA	GCC	AAC	GTT	TAT	GTT	ACA	GAA	1147
10	Lys	Gln	Ala	Phe	Gln	Ala	Thr	Val	Arg	Ala	Asn	Val	Tyr	Val	Thr	Glu	
215						220				225					230		
	AAT	GCG	GCC	ATC	GCC	TGC	CTG	TAT	GTG	GTG	TTA	GTG	GGA	GAA	ATG	CAA	1195
	Asn	Ala	Ala	Ile	Ala	Cys	Leu	Tyr	Val	Val	Leu	Val	Gly	Glu	Met	Gln	
					235					240					245		
15	GAG	CCC	ACT	GTG	CTG	CGG	CCT	GCC	GAC	CTT	GAA	AAG	CAG	CTG	TTT	TCT	
	Glu	Pro	Thr	Val	Leu	Arg	Pro	Ala	Asp	Leu	Glu	Lys	Gln	Leu	Phe	Ser	1243
				250					255						260		
20	CTG	CCA	CAC	TGG	AGG	ACA	GAT	GGG	CAC	CAC	GTC	ATT	ATC	AAC	CTG		1291
	Leu	Pro	His	Trp	Arg	Thr	Asp	Gly	His	Asn	His	Val	Ile	Ile	Asn	Leu	
			265					270									
	TCC	CGG	AAG	TCA	GAC	ACA	CAG	AAT	CTA	CTG	TAC	AAC	GTC	AGT	ACA	GGC	1339
25	Ser	Arg	Lys	Ser	Asp	Thr	Gln	Asn	Leu	Leu	Tyr	Asn	Val	Ser	Thr	Gly	
			280				285					290					
	CGC	CAT	GTG	GCC	CAG	TCC	ACC	CTC	TAT	GCT	GCC	CAG	TAC	AGA	GCT	GGC	1387
30	Arg	His	Val	Ala	Gln	Ser	Thr	Leu	Tyr	Ala	Ala	Gln	Tyr	Arg	Ala	Gly	
295						300				305					310		
	TTT	GAC	CTG	GTC	GTG	TCA	CCC	CTT	GTG	CAT	GCT	ATG	TCT	GAA	CCC	AAC	1435
	Phe	Asp	Leu	Val	Val	Ser	Pro	Leu	Val	His	Ala	Met	Ser	Glu	Pro	Asn	
					315					320					325		
35	TTC	ATG	GAA	ATC	CCA	CCG	CAG	GTG	CCA	GTT	AAG	CGG	AAA	TAT	CTC	TTC	1483
	Phe	Met	Glu	Ile	Pro	Pro	Gln	Val	Pro	Val	Lys	Arg	Lys	Tyr	Leu	Phe	
				330					335						340		
40	ACT	TTC	CAG	GGC	GAG	AAG	ATC	GAG	TCT	CTG	AGA	TCT	AGC	CTT	CAG	GAG	1531
	Thr	Phe	Gln	Gly	Glu	Lys	Ile	Glu	Ser	Leu	Arg	Ser	Ser	Leu	Gln	Glu	
				345				350					355				
	GCC	CGT	TCC	TTC	GAG	GAA	GAG	ATG	GAG	GGC	GAC	CCT	CCG	GCC	GAC	TAT	1579
45	Ala	Arg	Ser	Phe	Glu	Glu	Glu	Met	Glu	Gly	Asp	Pro	Pro	Ala	Asp	Tyr	
				360			365					370					
	GAC	GAT	CGC	ATC	ATT	GCC	ACC	CTA	AAG	GCT	GTA	CAG	GAC	AGC	AAG	CTG	1627
50	Asp	Asp	Arg	Ile	Ile	Ala	Thr	Leu	Lys	Ala	Val	Gln	Asp	Ser	Lys	Leu	
375						380					385					390	
	GAT	CAG	GTG	CTG	GTA	GAA	TTC	ACT	TGC	AAA	AAC	CAG	CCG	AAG	CCT	AGC	1675
	Asp	Gln	Val	Leu	Val	Glu	Phe	Thr	Cys	Lys	Asn	Gln	Pro	Lys	Pro	Ser	
					395					400					405		
55	CTG	CCG	ACT	GAG	TGG	GCA	CTG	TGT	GGG	GAG	CGG	GAA	GAC	CGC	CTG	GAG	1723
	Leu	Pro	Thr	Glu	Trp	Ala	Leu	Cys	Gly	Glu	Arg	Glu	Asp	Arg	Leu	Glu	
				410					415					420			
60	TTA	CTG	AAG	CTC	TCC	ACC	TTC	GCC	CTC	ATC	ATC	ACT	CCC	GGG	GAC	CCG	1771
	Leu	Leu	Lys	Leu	Ser	Thr	Phe	Ala	Leu	Ile	Ile	Thr	Pro	Gly	Asp	Pro	
				425				430						435			

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CGC	CTG	CTC	ATT	TCA	TCT	GGG	TGT	GCC	ACG	CGG	CTC	TTC	GAG	GCC	CTG	1819
Arg	Leu	Leu	Ile	Ser	Ser	Gly	Cys	Ala	Thr	Arg	Leu	Phe	Glu	Ala	Leu	
440						445										
5	GAG	GTG	GGG	GCC	GTG	CCG	GTG	GTG	CTC	GGG	GAG	CAG	GTG	CAG	CTC	1867
Glu	Val	Gly	Ala	Val	Pro	Val	Val	Val	Leu	Gly	Glu	Gln	Val	Gln	Leu	
455					460						465				Pro	470
10	TAC	CAC	GAC	ATG	CTG	CAG	TGG	AAC	GAG	GCC	GCC	CTG	GTG	GTG	CCC	1915
Tyr	His	Asp	Met	Leu	Gln	Trp	Asn	Glu	Ala	Ala	Ala	Leu	Val	Val	Pro	
				475						480					Lys	
15	CCT	CGC	GTC	ACA	GAG	GTC	CAC	TTC	CTG	TTA	CGA	AGT	CTT	TCA	GAC	1963
Pro	Arg	Val	Thr	Glu	Val	Val	His	Phe	Leu	Leu	Arg	Ser	Leu	Ser	Asp	
				490					495					500		
20	GAT	CTG	TTG	GCC	ATG	AGG	CGG	CAA	GGC	CGC	TTT	CTC	TGG	GAG	ACC	2011
Asp	Leu	Leu	Ala	Met	Arg	Arg	Arg	Gln	Gly	Arg	Phe	Leu	Trp	Glu	Thr	
			505					510					515		Tyr	
25	TTC	TCC	ACC	GCA	GAC	AGT	ATT	TTT	AAT	ACC	GTG	CTG	GCC	ATG	ATT	2059
Phe	Ser	Thr	Ala	Asp	Ser	Ser	Ile	Phe	Asn	Thr	Val	Leu	Ala	Met	Ile	
							525					530			Arg	
30	ACT	CGA	ATT	CAG	ATC	CCA	GCT	GCT	CCC	ATC	CGG	GAA	GAG	GTA	GCG	2107
Thr	Arg	Ile	Gln	Ile	Pro	Pro	Ala	Ala	Pro	Ile	Arg	Glu	Glu	Val	Ala	
535					540						545				550	
35	GAG	ATC	CCC	CAT	CGT	TCA	GGC	AAA	GCA	GCT	GGA	ACT	GAC	CCC	AAC	2155
Glu	Ile	Pro	His	Arg	Ser	Gly	Gly	Lys	Ala	Ala	Gly	Thr	Asp	Pro	Asn	
				555					560						565	
40	GCT	GAC	AAT	GGG	GAC	CTG	GAC	CTG	GGG	CCG	GTA	GAG	ACA	GAA	CCA	2203
Ala	Asp	Asn	Gly	Asp	Leu	Asp	Leu	Leu	Gly	Pro	Val	Glu	Thr	Glu	Pro	
			570					575						580		
45	TAT	GCC	TCA	CCT	AAA	TAC	CTC	CGC	AAT	TTC	ACT	CTG	ACT	GTC	ACA	2251
Tyr	Ala	Ser	Pro	Lys	Tyr	Leu	Leu	Arg	Asn	Phe	Thr	Leu	Thr	Val	Thr	
				585				590					595		Asp	
50	TGT	TAC	CGT	GGC	TGG	AAC	TCT	GCC	CCG	GGA	CGG	TTC	CAT	CTT	TTT	2299
Cys	Tyr	Arg	Gly	Trp	Asn	Ser	Ser	Ala	Pro	Gly	Arg	Phe	His	Leu	Phe	
				600		605						610			Pro	
55	CAC	ACA	CCC	TTT	GAT	CCT	GTG	TTG	CCC	TCT	GAG	GCC	AAA	TTC	TTG	2347
His	Thr	Pro	Phe	Asp	Pro	Pro	Val	Leu	Pro	Ser	Glu	Ala	Lys	Phe	Leu	
615					620						625				Gly	630
60	TCA	GGG	ACT	GGA	TTT	CGG	CCG	ATC	GGT	GGC	GGG	GCT	GGG	GGC	TCT	2395
Ser	Gly	Thr	Gly	Phe	Arg	Pro	Pro	Ile	Gly	Gly	Gly	Ala	Gly	Gly	Ser	
				635					640						645	
65	AAG	GAG	TTC	CAG	GCA	GCG	CTC	GGA	GGC	AAT	GTC	CAG	CGG	GAG	CAG	2443
Lys	Glu	Phe	Gln	Ala	Ala	Ala	Leu	Gly	Gly	Asn	Val	Gln	Arg	Glu	Gln	
			650					655						660	Phe	
70	ACA	GTT	GTG	ATG	CTG	ACC	TAC	GAG	CGG	GAG	GAA	GTG	CTC	ATG	AAC	2491
Thr	Val	Val	Met	Leu	Thr	Thr	Tyr	Glu	Arg	Glu	Glu	Val	Leu	Met	Asn	
			665					670					675		Ser	
80	CTG	GAG	AGA	CTC	AAC	GGC	CTC	CCC	TAC	CTG	AAC	AAG	GTA	GTG	GTG	2539
Leu	Glu	Arg	Leu	Asn	Gly	Gly	Leu	Pro	Tyr	Leu	Asn	Lys	Val	Val	Val	
							685					690				

	TGG AAC TCT CCC AAG CTG CCC TCG GAG GAC CTT TTG TGG CCA GAC ATT	2587
	Trp Asn Ser Pro Lys Leu Pro Ser Glu Asp Leu Leu Trp Pro Asp Ile	
	695 700 705 710	
5	GGT GTC CCC ATC ATG GTC GTC CGT ACT GAG AAG AAC AGT TTG AAC AAT	2635
	Gly Val Pro Ile Met Val Val Arg Thr Glu Lys Asn Ser Leu Asn Asn	
	715 720 725	
10	CGG TTC TTG CCC TGG AAT GAG ATT GAG ACA GAG GCC ATA CTG TCC ATC	2683
	Arg Phe Leu Pro Trp Asn Glu Ile Glu Thr Ala Ile Leu Ser Ile	
	730 735 740	
15	GAC GAT GAT GCT CAC CTC CGC CAT GAT GAA ATC ATG TTT GGG TTT TGG	2731
	Asp Asp Asp Ala His Leu Arg His Asp Glu Ile Met Phe Gly Phe Trp	
	745 750 755	
20	GTG TGG AGA GAA GCA CGT GAT CGC ATT GTG GGT TTC CCT GGC CGG TAC	2779
	Val Trp Arg Glu Ala Arg Asp Arg Ile Val Gly Phe Pro Gly Arg Tyr	
	760 765 770	
25	CAT GCG TGG GAC ATC CCG CAC CAG TCC TGG CTC TAC AAT TCC AAC TAC	2827
	His Ala Trp Asp Ile Pro His Gln Ser Trp Tyr Asn Ser Asn Tyr	
	775 780 785 790	
30	TCC TGT GAG CTG TCC ATG GTG CTG ACG GGC GCT GCC TTC TTT CAC AAG	2875
	Ser Cys Glu Leu Ser Met Val Leu Thr Gly Ala Ala Phe Phe His Lys	
	795 800 805	
35	TAT TAT GCC TAC CTG TAT TCT TAT GTG ATG CCC CAG GCC ATC CGG GAC	2923
	Tyr Tyr Ala Tyr Leu Tyr Ser Tyr Val Met Pro Gln Ala Ile Arg Asp	
	810 815 820	
40	ATG GTG GAC GAG TAC ATC AAC TGT GAG GAT ATC GCC ATG AAC TTC CTT	2971
	Met Val Asp Glu Tyr Ile Asn Cys Glu Asp Ile Ala Met Asn Phe Leu	
	825 830 835	
45	GTC TCC CAC ATC ACA CGG AAA CCC CCC ATC AAG GTG ACA TCA AGG TGG	3019
	Val Ser His Ile Thr Arg Lys Pro Pro Ile Lys Val Thr Ser Arg Trp	
	840 845 850	
50	ACT TTT CGA TGC CCA GGG TGC CCT CAG GCC CTG TCC CAT GAT GAC TCT	3067
	Thr Phe Arg Cys Pro Gly Cys Pro Gln Ala Leu Ser His Asp Asp Ser	
	855 860 865 870	
55	CAT TTT CAC GAG CGG CAC AAG TGT ATC AAC TTT TTT GTC AAG GTG TAC	3115
	His Phe His Glu Arg His Lys Cys Ile Asn Phe Phe Val Lys Val Tyr	
	875 880 885	
60	GGC TAT ATG CCT CTC TTG TAC ACA CAG TTC AGG GTG GAC TCC GTG CTC	3163
	Gly Tyr Met Pro Leu Leu Tyr Thr Gln Phe Arg Val Asp Ser Val Leu	
	890 895 900	
65	TTC AAG ACC CGC CTG CCC CAT GAC AAG ACC AAG TGC TTC AAG TTC ATC	3211
	Phe Lys Thr Arg Leu Pro His Asp Lys Thr Lys Cys Phe Lys Phe Ile	
	905 910 915	
70	TAGGGCCTTG CAGTTCTGAG GAGACAATGA GCAGAGCGAG GGGGAGTCAC CCTCAAGGTT	3271
	CCCAAGGTGT CGAAGGTCTCT TGGGGACATC TGTCGGGCAG GGCCAAGACC CTTTGCTGGG	3331
	AGAGGCAGCA GGAAGAGTGG AAAGGGATAG CTGCTTTTCA TTTTGAAGTC AGCCCACTG	3391
	GGCCTGGGAT CTTGCTCAGA GACTCAGGNC GTCTGCACAG GGCCTGACT GATAGCGAAC	3451

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3479

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gln Thr Cys Met Leu Arg Trp Ser Asn Arg Ile Arg Leu Thr Trp Leu
20 25 30

Tyr Tyr Leu Thr Thr Leu Asp Glu Ala Asp Glu Ala Gly Lys Arg Ile
25 50 55 60

Phe Gly Pro Arg Ala Gly Ser Glu Leu Cys Glu Val Lys His Val Leu
65 70 75 80

30Asp Leu Cys Arg Ile Arg Glu Ser Val Ser Glu Glu Leu Leu Gln Leu
85 90 95

Glu Ala Lys Arg Gln Glu Leu Asn Ser Glu Ile Ala Lys Leu Asn Leu
100 105 110

35 Lys Ile Glu Ala Cys Lys Lys Ser Ile Glu Asn Ala Lys Gln Asp Leu
115 120 125

Leu Gln Leu Lys Asn Val Ile Ser Gln Thr Glu His Ser Tyr Lys Glu
40 130 135 140

Leu Met Ala Gln Asn Gln Pro Lys Leu Ser Leu Pro Ile Arg Leu Leu
145 150 155 160

45Pro Glu Lys Asp Asp Ala Gly Leu Pro Pro Pro Lys Val Thr Arg Gly
165 170 175

Cys Arg Leu His Asn Cys Phe Asp Tyr Ser Arg Cys Pro Leu Thr Ser
180 185 190

50 Gly Phe Pro Val Tyr Val Tyr Asp Ser Asp Gln Phe Ala Phe Gly Ser
195 200 205

Tyr Leu Asp Pro Leu Val Lys Gln Ala Phe Gln Ala Thr Val Arg Ala
55 210 215 220

Asn Val Tyr Val Thr Glu Asn Ala Ala Ile Ala Cys Leu Tyr Val Val
225 230 235 240

60Leu Val Gly Glu Met Gln Glu Pro Thr Val Leu Arg Pro Ala Asp Leu
245 250 255

Glu Lys Gln Leu Phe Ser Leu Pro His Trp Arg Thr Asp Gly His Asn

		260						265						270					
	His	Val	Ile	Ile	Asn	Leu	Ser	Arg	Lys	Ser	Asp	Thr	Gln	Asn	Leu	Leu			
			275					280					285						
5	Tyr	Asn	Val	Ser	Thr	Gly	Arg	His	Val	Ala	Gln	Ser	Thr	Leu	Tyr	Ala			
		290					295					300							
10	Ala	Gln	Tyr	Arg	Ala	Gly	Phe	Asp	Leu	Val	Val	Ser	Pro	Leu	Val	His			
		305				310					315					320			
	Ala	Met	Ser	Glu	Pro	Asn	Phe	Met	Glu	Ile	Pro	Pro	Gln	Val	Pro	Val			
					325					330					335				
15	Lys	Arg	Lys	Tyr	Leu	Phe	Thr	Phe	Gln	Gly	Glu	Lys	Ile	Glu	Ser	Leu			
				340					345					350					
	Arg	Ser	Ser	Leu	Gln	Glu	Ala	Arg	Ser	Phe	Glu	Glu	Glu	Met	Glu	Gly			
			355					360					365						
20	Asp	Pro	Pro	Ala	Asp	Tyr	Asp	Asp	Arg	Ile	Ile	Ala	Thr	Leu	Lys	Ala			
							375					380							
	Val	Gln	Asp	Ser	Lys	Leu	Asp	Gln	Val	Leu	Val	Glu	Phe	Thr	Cys	Lys			
	25	385				390					395					400			
	Asn	Gln	Pro	Lys	Pro	Ser	Leu	Pro	Thr	Glu	Trp	Ala	Leu	Cys	Gly	Glu			
					405					410					415				
30	Arg	Glu	Asp	Arg	Leu	Glu	Leu	Lys	Leu	Ser	Ser	Thr	Phe	Ala	Leu	Ile			
				420					425					430					
	Ile	Thr	Pro	Gly	Asp	Pro	Arg	Leu	Leu	Ile	Ser	Ser	Gly	Cys	Ala	Thr			
				435				440					445						
35	Arg	Leu	Phe	Glu	Ala	Leu	Glu	Val	Gly	Ala	Val	Pro	Val	Val	Leu	Gly			
		450					455					460							
	Glu	Gln	Val	Gln	Leu	Pro	Tyr	His	Asp	Met	Leu	Gln	Trp	Asn	Glu	Ala			
	40	465				470					475					480			
	Ala	Leu	Val	Val	Pro	Lys	Pro	Arg	Val	Thr	Glu	Val	His	Phe	Leu	Leu			
					485					490					495				
45	Arg	Ser	Leu	Ser	Asp	Ser	Asp	Leu	Leu	Ala	Met	Arg	Arg	Gln	Gly	Arg			
				500					505					510					
	Phe	Leu	Trp	Glu	Thr	Tyr	Phe	Ser	Thr	Ala	Asp	Ser	Ile	Phe	Asn	Thr			
			515					520					525						
50	Val	Leu	Ala	Met	Ile	Arg	Thr	Arg	Ile	Gln	Ile	Pro	Ala	Ala	Pro	Ile			
		530					535					540							
	Arg	Glu	Glu	Val	Ala	Ala	Glu	Ile	Pro	His	Arg	Ser	Gly	Lys	Ala	Ala			
	55	545				550					555					560			
	Gly	Thr	Asp	Pro	Asn	Met	Ala	Asp	Asn	Gly	Asp	Leu	Asp	Leu	Gly	Pro			
					565					570					575				
60	Val	Glu	Thr	Glu	Pro	Pro	Tyr	Ala	Ser	Pro	Lys	Tyr	Leu	Arg	Asn	Phe			
				580					585					590					
	Thr	Leu	Thr	Val	Thr	Asp	Cys	Tyr	Arg	Gly	Trp	Asn	Ser	Ala	Pro	G			

595 600 605

Arg Phe His Leu Phe Pro His Thr Pro Phe Asp Pro Val Leu Pro Ser
610 615 620

5
Glu Ala Lys Phe Leu Gly Ser Gly Thr Gly Phe Arg Pro Ile Gly Gly
625 630 635 640

10
Gly Ala Gly Gly Ser Gly Lys Glu Phe Gln Ala Ala Leu Gly Gly Asn
645 650 655

Val Gln Arg Glu Gln Phe Thr Val Val Met Leu Thr Tyr Glu Arg Glu
660 665 670

15
Glu Val Leu Met Asn Ser Leu Glu Arg Leu Asn Gly Leu Pro Tyr Leu
675 680 685

Asn Lys Val Val Val Val Trp Asn Ser Pro Lys Leu Pro Ser Glu Asp
690 695 700

20
Leu Leu Trp Pro Asp Ile Gly Val Pro Ile Met Val Val Arg Thr Glu
705 710 715 720

25
Lys Asn Ser Leu Asn Asn Arg Phe Leu Pro Trp Asn Glu Ile Glu Thr
725 730 735

Glu Ala Ile Leu Ser Ile Asp Asp Ala His Leu Arg His Asp Glu
740 745 750

30
Ile Met Phe Gly Phe Trp Val Trp Arg Glu Ala Arg Asp Arg Ile Val
755 760 765

Gly Phe Pro Gly Arg Tyr His Ala Trp Asp Ile Pro His Gln Ser Trp
770 775 780

35
Leu Tyr Asn Ser Asn Tyr Ser Cys Glu Leu Ser Met Val Leu Thr Gly
785 790 795 800

40
Ala Ala Phe Phe His Lys Tyr Tyr Ala Tyr Leu Tyr Ser Tyr Val Met
805 810 815

Pro Gln Ala Ile Arg Asp Met Val Asp Glu Tyr Ile Asn Cys Glu Asp
820 825 830

45
Ile Ala Met Asn Phe Leu Val Ser His Ile Thr Arg Lys Pro Pro Ile
835 840 845

Lys Val Thr Ser Arg Trp Thr Phe Arg Cys Pro Gly Cys Pro Gln Ala
850 855 860

50
Leu Ser His Asp Asp Ser His Phe His Glu Arg His Lys Cys Ile Asn
865 870 875 880

55
Phe Phe Val Lys Val Tyr Gly Tyr Met Pro Leu Leu Tyr Thr Gln Phe
885 890 895

Arg Val Asp Ser Val Leu Phe Lys Thr Arg Leu Pro His Asp Lys Thr
900 905 910

60
Lys Cys Phe Lys Phe Ile
915

(2) INFORMATION FOR SEQ ID NO:3:

	Ala	Lys	Arg	Gln	Glu	Leu	Asn	Ser	Glu	Ile	Ala	Lys	Leu	Asn	Leu	Lys		
					1020						1025				1030			
	ATC	GAA	GCC	TGT	AAG	AAG	AGC	ATT	GAG	AAC	GCC	AAG	CAG	GAC	CTG	CTC		980
5	File	Glu	Ala	Cys	Lys	Lys	Ser	Ile	Glu	Asn	Ala	Lys	Gln	Asp	Leu	Leu		
				1035					1040				1045					
	CAG	CTC	AAG	AAT	GTC	ATC	AGC	CAG	ACC	GAG	CAT	TCC	TAC	AAG	GAG	CTC		1028
10	Gln	Leu	Lys	Lys	Asn	Val	Ile	Ser	Gln	Thr	Glu	His	Ser	Lys	Lys	Leu		
			1050					1055					1060					
	ATG	GCC	CAG	AAC	CAG	CCC	AAG	CTG	TCC	CTG	CCC	ATC	CGA	CTG	CTC	CCA		1076
15	Met	Ala	Gln	Asn	Gln	Pro	Lys	Leu	Ser	Leu	Pro	Ile	Arg	Leu	Leu	Pro		
			1065				1070					1075						
	GAG	AAG	GAC	GAT	GCC	GGC	CTC	CCT	CCC	CCG	AAG	GCC	ACT	CGG	GGC	TGC		1124
	Glu	Lys	Asp	Asp	Ala	Gly	Leu	Pro	Pro	Pro	Lys	Ala	Thr	Arg	Gly	Cys		
			1080		1085						1090				1095			
20	CGG	CTA	CAC	AAC	TGC	TTT	GAT	TAT	TCT	CGT	TGC	CCT	CTC	ACC	TCT	GGC		1172
	Arg	Leu	His	Asn	Cys	Phe	Asp	Tyr	Ser	Arg	Cys	Pro	Leu	Thr	Ser	Gly		
				1100						1105					1110			
	TTC	CCG	GTC	TAC	GTC	TAT	GAC	AGT	GAC	CAG	TTT	GTC	TTT	GGC	AGC	TAC		1220
25	Phe	Pro	Val	Tyr	Val	Tyr	Asp	Ser	Asp	Gln	Phe	Val	Phe	Gly	Ser	Tyr		
				1115					1120					1125				
	CTG	GAT	CCC	TTG	GTC	AAG	CAG	GCT	TTT	CAG	GCG	ACA	GCA	CGA	GCT	AAC		1268
30	Leu	Asp	Pro	Leu	Val	Lys	Gln	Ala	Phe	Gln	Ala	Thr	Ala	Arg	Ala	Asn		
				1130			1135						1140					
	GTT	TAT	GTT	ACA	GAA	AAT	GCA	GAC	ATC	GCC	TGC	CTT	TAC	GTG	ATA	CTA		1316
35	Val	Tyr	Val	Thr	Glu	Asn	Ala	Asp	Ile	Ala	Cys	Leu	Tyr	Val	Ile	Leu		
				1145			1150					1155						
	GTG	GGA	GAG	ATG	CAG	GAG	CCC	GTG	GTG	CTG	CGG	CCT	GCT	GAG	CTG	GAG		1364
	Val	Gly	Glu	Met	Gln	Glu	Pro	Val	Val	Leu	Arg	Pro	Ala	Glu	Leu	Glu		
				1160		1165				1170					1175			
40	AAG	CAG	TTG	TAT	TCC	CTG	CCA	CAC	TGG	CGG	ACG	GAT	GGA	CAC	AAC	CAT		1412
	Lys	Gln	Leu	Tyr	Ser	Leu	Pro	His	Trp	Arg	Thr	Asp	Gly	His	Asn	His		
					1180					1185				1190				
	GTC	ATC	ATC	AAT	CTG	TCA	CGT	AAG	TCA	GAT	ACA	CAG	AAC	CTT	CTC	TAT		1460
45	Val	Ile	Ile	Asn	Leu	Ser	Arg	Lys	Ser	Asp	Thr	Gln	Asn	Leu	Leu	Tyr		
				1195					1200					1205				
	AAC	GTC	AGT	ACT	GGC	CGT	GCC	ATG	GTG	GCC	CAG	TCC	ACC	TTC	TAC	ACT		1508
50	Asn	Val	Ser	Thr	Gly	Arg	Ala	Met	Val	Ala	Gln	Ser	Thr	Phe	Thr	Thr		
				1210				1215					1220					
	GTC	CAG	TAC	AGA	CCT	GGC	TTT	GAC	TTG	GTC	GTA	TCA	CCG	CTG	GTC	CAT		1556
55	Val	Gln	Tyr	Arg	Pro	Gly	Phe	Asp	Leu	Val	Val	Ser	Pro	Leu	Val	His		
				1225			1230					1235						
	GCC	ATG	TCT	GAG	CCC	AAC	TTC	ATG	GAA	ATC	CCA	CCA	CAG	GTG	CCG	GTG		1604
	Ala	Met	Ser	Glu	Pro	Asn	Phe	Met	Glu	Ile	Pro	Pro	Gln	Val	Pro	Val		
				1240		1245					1250				1255			
60	AAG	CGG	AAA	TAT	CTC	TTC	ACC	TTC	CAG	GGC	GAG	AAG	ATT	GAG	TCT	CTG		1652
	Lys	Arg	Lys	Tyr	Leu	Phe	Thr	Phe	Gln	Gly	Glu	Lys	Ile	Glu	Ser	Leu		
					1260					1265					1270			

AGG TCT AGC CTT	TAG GAG GCC CGC TCC TTC GAA GAG GAA ATG GAG GGC	1700
Arg Ser Ser	Leu Gln Glu Ala Arg Ser Phe Glu Glu Glu Thr Leu Glu Gly	
1275	1280	1285
5GAC CCT CCC GCC GAC TAC GAT GAC CGG ATC ATT GCC ACC CTG AAG GCG	1748	
Asp Pro Pro	Ala Asp Tyr Asp Arg Ile Ile Ala Thr Leu Lys Ala	
1290	1295	1300
GTG CAG GAC AGC AAG CTG GAT CAG GTC CTG GTG GAA TTC ACC TGC AAA	1796	
10Val Gln Asp Ser Lys Leu Asp Gln Val Leu Val Glu Phe Thr Cys Lys		
1305	1310	1315
AAC CAG CCC AAA CCC AGC CTG CCG ACT GAG TGG GCA CTG TGT GGA GAG	1844	
Asn Gln Pro Lys Pro Ser Leu Pro Thr Glu Trp Ala Leu Cys Gly Glu		
151320	1325	1330
CGG GAG GAC CGC TTG GAA TTG CTG AAG CTC TCC ACC TTC GCC CTC ATC	1892	
Arg Glu Asp Arg	Leu Glu Leu Leu Lys Leu Ser Thr Phe Ala Leu Ile	
1340	1345	1350
20 ATT ACC CCC GGG GAC CCT CGC TTG GTT ATT TCC TCT GGG TGT GCA ACA	1940	
Ile Thr Pro Gly Asp Pro Arg Leu Val Ile Ser Ser Gly Cys Ala Thr		
1355	1360	1365
25CGG CTC TTC GAA GCC CTG GAA GTC GGT GCC GTC CCG GTG GTG CTG GGG	1988	
Arg Leu Phe Glu Ala Leu Glu Val Gly Ala Val Pro Val Val Leu Gly		
1370	1375	1380
GAG CAG GTC CAG CTT CCC TAC CAG GAC ATG CTG CAG TGG AAC GAG GCG	2036	
30Glu Gln Val Gln Leu Pro Tyr Gln Asp Met Leu Gln Trp Asn Glu Ala		
1385	1390	1395
GCC CTG GTG GTG CCA AAG CCT CGT GTT ACC GAG GTT CAT TTC CTG CTC	2084	
351400 Ala Leu Val Val Pro Lys Pro Arg Val Thr Glu Val His Phe Leu Leu		
1405	1410	1415
AGA AGC CTC TCC GAT AGT GAC CTC CTG GCT ATG AGG CGG CAA GGC CGC	2132	
Arg Ser Leu Ser Asp Ser Asp Leu Leu Ala Met Arg Arg Gln Gly Arg		
1420	1425	1430
40 TTT CTC TGG GAG ACT TAC TTC TCC ACT GCT GAC AGT ATT TTT AAT ACC	2180	
Phe Leu Trp Glu Thr Tyr Phe Ser Thr Ala Asp Ser Ile Phe Asn Thr		
1435	1440	1445
45GTG CTG GCT ATG ATT AGG ACT CGC ATC CAG ATC CCA GCC GCT CCC ATC	2228	
Val Leu Ala Met Ile Arg Thr Arg Ile Gln Ile Pro Ala Ala Pro Ile		
1450	1455	1460
CGG GAA GAG GCG GCA GCT GAG ATC CCC CAC CGT TCA GGC AAG GCG GCT	2276	
50Arg Glu Glu Ala Ala Ala Glu Ile Pro His Arg Ser Gly Lys Ala Ala		
1465	1470	1475
GGA ACT GAC CCC AAC ATG GCT GAC AAC GGG GAC CTG GAC CTG GGG CCA	2324	
551480 Gly Thr Asp Pro Asn Met Ala Asp Asn Gly Asp Leu Asp Leu Gly Pro		
1485	1490	1495
GTG GAG ACG GAG CCG CCC TAC GCC TCA CCC AGA TAC CTC CGC AAT TTC	2372	
Val Glu Thr Glu Pro Pro Tyr Ala Ser Pro Arg Tyr Leu Arg Asn Phe		
1500	1505	1510
60 ACT CTG ACT GTC ACT GAC TTT TAC CGC AGC TGG AAC TGT GCT CCA GGG	2420	
Thr Leu Thr Val Thr Asp Phe Tyr Arg Ser Trp Asn Cys Ala Pro Gly		
1515	1520	1525

	CTC	TTC	CAT	CTT	TTC	CCC	CAC	ACT	CCC	TTT	GAC	CCT	GTG	TTG	CCC	TCA	2468
	Pro	Phe	His	Leu	Phe	Pro	His	Thr	Pro	Phe	Asp	Pro	Val	Leu	Pro	Ser	
			1530					1535					1540				
5	GAG	GCC	AAA	TTC	TTG	GGC	TCA	GGG	ACT	GGC	TTT	CGG	CCT	ATT	GGT	GGT	2516
	Ala	Ala	Lys	Phe	Leu	Gly	Ser	Gly	Thr	Gly	Phe	Arg	Pro	Ile	Gly	Gly	
			1545				1550					1555					
10	GGA	GCT	GGG	GGT	TCT	GGC	AAG	GAA	TTT	CAG	GCA	GCG	CTT	GGA	GGC	AAT	2564
	Gly	Ala	Gly	Gly	Ser	Gly	Lys	Glu	Phe	Gln	Ala	Ala	Leu	Gly	Gly	Asn	
			1560				1565				1570					1575	
15	GTT	CCC	CGA	GAG	CAG	TTC	ACG	GTG	GTG	ATG	TTG	ACT	TAT	GAG	CGG	GAG	2612
	Val	Pro	Arg	Glu	Gln	Phe	Thr	Val	Val	Met	Leu	Thr	Tyr	Glu	Arg	Glu	
					1580					1585					1590		
20	GAA	GTG	CTT	ATG	AAC	TCT	TTA	GAG	AGG	CTG	AAT	GGC	CTC	CCT	TAC	CTG	2660
	Glu	Val	Leu	Met	Asn	Ser	Leu	Glu	Arg	Leu	Asn	Gly	Leu	Pro	Tyr	Leu	
				1595					1600					1605			
25	AAC	AAG	GTC	GTG	GTG	GTG	TGG	AAT	TCT	CCC	AAG	CTG	CCA	TCA	GAG	GAC	2708
	Asn	Lys	Val	Val	Val	Val	Trp	Asn	Ser	Pro	Lys	Leu	Pro	Ser	Glu	Asp	
		--		1610				1615					1620				
25	CTT	CTG	TGG	CCT	GAC	ATT	GGC	GTT	CCC	ATC	ATG	GTG	GTC	CGT	ACT	GAG	2756
	Leu	Leu	Trp	Pro	Asp	Ile	Gly	Val	Pro	Ile	Met	Val	Val	Arg	Thr	Glu	
			1625				1630					1635					
30	AAG	AAC	AGT	TTG	AAC	AAC	CGA	TTC	TTA	CCC	TGG	AAT	GAA	ATT	GAG	ACA	2804
	Lys	Asn	Ser	Leu	Asn	Asn	Arg	Phe	Leu	Pro	Trp	Asn	Glu	Ile	Glu	Thr	
			1640				1645				1650					1655	
35	GAG	GCC	ATC	CTG	TCC	ATT	GAT	GAC	GAT	GCT	CAC	CTC	CGC	CAT	GAC	GAA	2852
	Glu	Ala	Ile	Leu	Ser	Ile	Asp	Asp	Asp	Ala	His	Leu	Arg	His	Asp	Glu	
					1660					1665					1670		
40	ATC	ATG	TTT	GGG	TTC	CGG	GTG	TGG	AGA	GAA	GCT	CGG	GAC	CGC	ATC	GTG	2900
	Ile	Met	Phe	Gly	Phe	Arg	Val	Trp	Arg	Glu	Ala	Arg	Asp	Arg	Ile	Val	
				1675					1680						1685		
45	GGC	TTC	CCT	GGC	CGT	TAC	CAC	GCA	TGG	GAC	ATC	CCC	CAT	CAG	TCC	TGG	2948
	Gly	Phe	Pro	Gly	Arg	Tyr	His	Ala	Trp	Asp	Ile	Pro	His	Gln	Ser	Trp	
			1690					1695					1700				
45	CTC	TAC	AAC	TCC	AAC	TAC	TCC	TGT	GAG	CTG	TCC	ATG	GTG	CTG	ACA	GGT	2996
	Leu	Tyr	Asn	Ser	Asn	Tyr	Ser	Cys	Glu	Leu	Ser	Met	Val	Leu	Thr	Gly	
			1705				1710					1715					
50	GCT	GCC	TTC	TTT	CAC	AAG	TAT	TAT	GCC	TAC	CTG	TAT	TCT	TAT	GTG	ATG	3044
	Ala	Ala	Phe	Phe	His	Lys	Tyr	Tyr	Ala	Tyr	Leu	Tyr	Ser	Tyr	Val	Met	
			1720				1725				1730					1735	
55	CCC	CAG	GCC	ATC	CGG	GAC	ATG	GTG	GAT	GAA	TAC	ATC	AAC	TGT	GAG	GAC	3092
	Pro	Gln	Ala	Ile	Arg	Asp	Met	Val	Asp	Glu	Tyr	Ile	Asn	Cys	Glu	Asp	
				1740						1745					1750		
60	ATT	GCC	ATG	AAC	TTC	CTT	GTC	TCC	CAC	ATC	ACT	CGG	AAG	CCC	CCC	ATC	3140
	Ile	Ala	Met	Asn	Phe	Leu	Val	Ser	His	Ile	Thr	Arg	Lys	Pro	Pro	Ile	
				1755					1760					1765			
60	AAG	GTG	ACC	TCA	CGG	TGG	ACA	TTC	CGA	TGC	CCA	GGA	TGC	CCT	CAG	GCC	3188
	Lys	Val	Thr	Ser	Arg	Trp	Thr	Phe	Arg	Cys	Pro	Gly	Cys	Pro	Gln	Ala	
			1770					1775					1780				

	CTG	TCT	CAT	GAT	GAC	TCC	CAC	TTC	CAC	GAG	CGG	CAC	AAG	TGC	ATC	AAC	3236
	Leu	Ser	His	Asp	Asp	Ser	His	Phe	His	Glu	Arg	His	Lys	Cys	Ile	Asn	
	1785						1790					1795					
5	TTC	TTC	GTG	AAG	GTG	TAC	GGC	TAC	ATG	CCC	CTC	CTG	TAC	ACG	CAG	TTC	3284
	Phe	Phe	Val	Lys	Val	Tyr	Gly	Tyr	Met	Pro	Leu	Leu	Tyr	Thr	Gln	Phe	
	1800					1805					1810				1815		
	AGG	GTG	GAT	TCT	GTG	CTC	TTC	AAG	ACA	CGC	CTG	CCC	CAT	GAC	AAG	ACC	3332
10	Arg	Val	Asp	Ser	Val	Leu	Phe	Lys	Thr	Arg	Leu	Pro	His	Asp	Lys	Thr	
					1820					1825					1830		
	AAG	TGC	TTC	AAG	TTC	ATC	TAGGGGCGACG	GCACGGTCTG	GGGAAGAGGA								3380
15	Lys	Cys	Phe	Lys	Phe	Ile											
	1835																
	TGAGCAGAGG	GAGGAAGATG	GCTCCCAAGG	TTCCTAGGCA	TTGCAGGACC	TTGGGCACAT											3440
	CTGCTGGTGG	GTGGCCCAAG	GCCTCTGCTG	GAAGGGGCGAG	CAGGAGGAGT	GGAAGGAAAC											3500
20	CGCTGCCTTT	ATCTTGAAGT	CAGCCCACT	GGSCCTGGAG	CCCTGGGCGG	AGTCCCCGGG											3560
	GTTCCCCACA	CAGGGCACTG	ACTGATAGCT	TACACTGAGG	ACTGTGGCGA	CTCTGCAGAG											3620
25	TCACTCACAC	CGTTCTGACG	CCCAGGACAG	CTGGTTCTGG	GTTTTTACAT	TCAATAACAA											3680
	CTATTATGAT	TATTTAAAAA	GAGAAAGTTT	CAGATTTGCC	ATTCAAGGCT	TATTTATATA											3740
	TATGTGTGTG	TATATAAATA	CATGCACACA	CTTGCATACA	TATATATTTT	TGGCTGGGGG											3800
30	AGTGTGAGTT	TTGCCTTTCT	AAGGGAGGGA	CCGCGCAGGC	TCCTTTGTTT	TGTATTCTGG											3860
	CGGAGATGGG	TCCTGGCCTT	GTGTCACTGG	CTTATCCTTA	AAGATCATCT	CCCATCCTCC											3920
35	CCAGCGCCAT	CTGTGTGCAG	CAACCAGAAA	GGGATGAAT	TGGCCCTCTT	CGGGGCCTGG											3980
	ACAAGGCTCT	TTCCTTACCC	TTTCTGTGTG	CAGTCAGCAA	CGCTGTAATC	ACATTCTCTT											4040
	CCCAGTGAAT	CCCTGGGAGC	GCCTGACCTT	GGTGGGCTGT	TCAGCTTCTT	GCTGCTGGGG											4100
40	CCAGCGATTT	TTGAGGATTT	ATCTTTAGGC	CAGGCTTGCC	TCCGTACTTA	TCCTGTCTCT											4160
	CCCATTCTCT	TCTTGTTTGA	GAGAGAATGA	GGAAGCAAA	AGTGAGAAAG	AATAGGGGCT											4220
45	GAGACGCCA	CTCCAGATG	GCTCTTTCTA	TCCTGCTCTT	CTGTTGAAAC	ACACGTGCTG											4280
	TGGGCCCTCAG	CGCTTTCTGA	AGTGCTCTTT	CTTGGATTGG	ACAGAGAGATC	AGCAGCGTGC											4340
	ACATCTGCTG	TGGTCTGAAG	TGGTTTGCAG	GTACAGCTCC	TCTCCCTAGT	GTAGAGCAAG											4400
50	CCAGTGTCTT	TCGAGGAACC	CACCCGGCTG	GCCGGGAAGT	TTTACAGCAA	GGCGCTGCC											4460
	TTGGGATAAT	TCCTTGGTGA	AATTACACCT	CCCCCGCCT	CTGTCTGGAG	CCCCATCTCT											4520
55	TGTTATCTGT	GGTTTTTGGG	CCCCTAATGT	CAGCTTGGCT	GTAGAGCTCC	CCGAGGTTTG											4580
	GTATGTGCTA	GAACAATGGG	AGGCTGTGAT	TTGCTGTGTA	AGCTCACATC	CAGCCTTGGA											4640
	ATCTAACGGG	CATTACAAC	CCGAGTTACC	ACTTTCCACT	CCCTGCTTAG	GATTCTGTTC											4700
60	CCTGGGCTGA	AACTGAAATA	AGCTAATTTT	TTGGGTCACG	GTGGCAGTAG	GGGAACCTAG											4760
	GAGGGTGTGA	GTGGCATTTG	TCAGGGATTT	AGCCCATGAC	GTGTTTCTTG	AACCCCTACTT											4820

TCTGGAAGTG GAGTTGACTC TGGAAATTTT CTAGCAACTG AACAAAAGCT CAGGTTTGTC 4880
 CTGGTCATGC ACATGCGCTTA AGCCAGTTCC GTCTTCCCTA GACCTTGSCA TCCTGTGCTT 4940
 5 CTATTTCTTG GAATACGTTC TCCTCTGACC TGCCGTGTACC ACGTGGGTCC TCTTCAAGTA 5000
 CTGTTTGA GCTGGGCTCT TTTGTGTAGC TCCCACCCAC CTGTAGGGCT AGCTCGGGCT 5060
 AAGGGAAC TCCCCATTGG CAAACCGGAC CCGGCCGCGC CCGAGACTGT GTTTCCAAAG 5120
 10 GTTCCCGCC CCCAACCCCA GCATCAGCCT GTAGCTCCCC TGCTGAGGCA GTGTGCTTAT 5180
 GTTCCAGCA GTGGGGGTCA GACGCCCTTC CTCAGAACTT TCTAGTTGCC CTCTACCTGA 5240
 15 CTCTGACTT GTATTCTTT TAGCAGTAGC CTCTTCCCT CCGGGAGCCA AAGAGTGTGG 5300
 TGTGTGGCG TATATTGTGG CTGCTATTTC ATCTGGTTTC TTTAATGTG AGGAACCTAC 5360
 ATACTGACTT CAGTGGGACT CGGTGAGCCG GGGCCGTCTG TGTGTGGGA CCCCTTTAG 5420
 20 CGGGACTCAG TGAGCTGGG CCGTCTGTGT GGTGGAGCCA GGGCTCTCC CTTTAGTGG 5480
 GCCAGTTGT CGGGCCCCGA ATGTCACTGG TGGATCTAAG AAGGGCTGAG TGGCTGACA 5540
 25 CCAAAACATG CCGCAGGAG GCGTGTGGT CCGGTGCTTC CAACAAGGAC AGCCCTCCTT 5600
 GACCTGAAA GGAACACTGG CTTGAAGGAC TGCAGACAGG CTCTAGGGG CACGCCCTCC 5660
 TCAGCGAGAG GCGCAAGGT GGCACAGTG TCACTGGTCA GGTGCTCTC ACCACGGGA 5720
 30 AGCGCCGAC CTGTGACTCG CTTGAGATGG GAAAGCGGCG CCACAGACCC CGGCTCTCCT 5780
 TGGCTGTCTG TGGGCCGCC CTGGCCACCT TGTCTGGCT CCGAGGGTG AGGAGCGCCT 5840
 35 CGTCTCTGG GTGGCCGGCT TGCTGCTCCG GTTGGGCTG TCTTACCATA ACACCGTCCC 5900
 AGGGCTCTGC AGGCCACTGT GAGCGCTGGC TCCCTGGGCA GTGCTCTCC GTGTGGACTG 5960
 TGCCCTAGGC CAGGGCTCAC CAGCTGGGT CCTGTCCGA AGGATGGGAT CTTTCTGGGA 6020
 40 GCTGCGCCG ACAGAGTGG GAGCTCCTAG TTTGTGGGG GAAGCTTTGA TATCCATGCC 6080
 ACGTCCATCC ACCCCACCCC TTTTCTCAC GAGCACAATG GTCTTACATT GGATTTTGT 6140
 45 AAAAAAATAA AATAAATGG AGACTTTAAC TC 6172

(2) INFORMATION FOR SEQ ID NO:4:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 919 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 55 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Gly Tyr Thr Met Leu Arg Asn Gly Gly Ala Gly Asn Gly Gly
 60 1 5 10 15
 Gln Thr Cys Met Leu Arg Trp Ser Asn Arg Ile Arg Leu Thr Trp Leu
 20 25 30

	Ser	Phe	Thr	Leu	Phe	Val	Ile	Leu	Val	Phe	Phe	Pro	Leu	Ile	Ala	His
			35						40					45		
5	Tyr	Tyr	Leu	Thr	Thr	Leu	Asp	Glu	Ala	Asp	Glu	Ala	Gly	Lys	Arg	Ile
		50					55					60				
	Phe	Gly	Pro	Arg	Val	Gly	Asn	Glu	Leu	Cys	Glu	Val	Lys	His	Val	Leu
	65					70					75					80
10	Asp	Leu	Cys	Arg	Ile	Arg	Glu	Ser	Val	Ser	Glu	Glu	Leu	Leu	Gln	Leu
					85					90					95	
	Glu	Ala	Lys	Arg	Gln	Glu	Leu	Asn	Ser	Glu	Ile	Ala	Lys	Leu	Asn	Leu
					100				105					110		
15	Lys	Ile	Glu	Ala	Cys	Lys	Lys	Ser	Ile	Glu	Asn	Ala	Lys	Gln	Asp	Leu
			115					120					125			
20	Leu	Gln	Leu	Lys	Asn	Val	Ile	Ser	Gln	Thr	Glu	His	Ser	Tyr	Lys	Glu
		130					135					140				
	Leu	Met	Ala	Gln	Asn	Gln	Pro	Lys	Leu	Ser	Leu	Pro	Ile	Arg	Leu	Leu
	145					150					155					160
25	Pro	Glu	Lys	Asp	Asp	Ala	Gly	Leu	Pro	Pro	Pro	Lys	Ala	Thr	Arg	Gly
					165					170					175	
	Cys	Arg	Leu	His	Asn	Cys	Phe	Asp	Tyr	Ser	Arg	Cys	Pro	Leu	Thr	Ser
				180					185					190		
30	Gly	Phe	Pro	Val	Tyr	Val	Tyr	Asp	Ser	Asp	Gln	Phe	Val	Phe	Gly	Ser
			195					200					205			
35	Tyr	Leu	Asp	Pro	Leu	Val	Lys	Gln	Ala	Phe	Gln	Ala	Thr	Ala	Arg	Ala
			210				215					220				
	Asn	Val	Tyr	Val	Thr	Glu	Asn	Ala	Asp	Ile	Ala	Cys	Leu	Tyr	Val	Ile
	225					230				235						240
40	Leu	Val	Gly	Glu	Met	Gln	Glu	Pro	Val	Val	Leu	Arg	Pro	Ala	Glu	Leu
					245					250					255	
	Glu	Lys	Gln	Leu	Tyr	Ser	Leu	Pro	His	Trp	Arg	Thr	Asp	Gly	His	Asn
				260					265					270		
45	His	Val	Ile	Ile	Asn	Leu	Ser	Arg	Lys	Ser	Asp	Thr	Gln	Asn	Leu	Leu
			275					280					285			
50	Tyr	Asn	Val	Ser	Thr	Gly	Arg	Ala	Met	Val	Ala	Gln	Ser	Thr	Phe	Tyr
		290					295					300				
	Thr	Val	Gln	Tyr	Arg	Pro	Gly	Asp	Leu	Val	Val	Ser	Pro	Leu	Val	
	305					310					315				320	
55	His	Ala	Met	Ser	Glu	Pro	Asn	Phe	Met	Glu	Ile	Pro	Pro	Gln	Val	Pro
					325					330					335	
	Val	Lys	Arg	Lys	Tyr	Leu	Phe	Thr	Phe	Gln	Gly	Glu	Lys	Ile	Glu	Ser
				340					345					350		
60	Leu	Arg	Ser	Ser	Leu	Gln	Glu</									

10	Gly 370	Asp 375	Pro	Pro	Ala	Asp 375	Tyr 375	Asp 375	Asp 375	Arg 375	Ile 380	Ile 380	Ala 380	Thr 380	Leu 380	Lys 380
15	Ala 5385	Val 5385	Gln 5385	Asp 5385	Ser 5385	Lys 390	Leu 390	Asp 390	Gln 390	Val 390	Leu 395	Val 395	Glu 395	Phe 395	Thr 395	Cys 400
20	Lys 405	Asn 405	Gln 405	Pro 405	Lys 405	Pro 405	Ser 405	Leu 405	Pro 410	Thr 410	Glu 410	Trp 410	Ala 415	Leu 415	Cys 415	Gly 415
25	Glu 420	Arg 420	Glu 420	Asp 420	Arg 420	Leu 420	Glu 425	Leu 425	Lys 425	Leu 425	Ser 425	Thr 425	Phe 430	Ala 430	Leu 430	Lys 430
30	Ile 435	Ile 435	Thr 435	Pro 435	Gly 435	Asp 435	Pro 440	Arg 440	Leu 440	Val 440	Ile 440	Ser 445	Ser 445	Gly 445	Cys 445	Ala 445
35	Thr 450	Arg 450	Leu 450	Phe 450	Glu 450	Ala 455	Leu 455	Glu 455	Val 455	Gly 455	Ala 460	Val 460	Pro 460	Val 460	Val 460	Leu 460
40	Gly 20465	Glu 20465	Gln 20465	Val 20465	Gln 20465	Leu 20465	Pro 20465	Tyr 20465	Gln 20465	Asp 20465	Met 20465	Leu 20465	Gln 20465	Trp 20465	Asn 20465	Glu 20465
45	Ala 480	Ala 480	Leu 480	Val 480	Val 485	Pro 485	Lys 485	Pro 485	Arg 490	Val 490	Thr 490	Glu 490	Val 495	His 495	Phe 495	Leu 495
50	Leu 500	Arg 500	Ser 500	Leu 500	Ser 500	Asp 500	Ser 505	Asp 505	Leu 505	Leu 505	Ala 505	Met 505	Arg 510	Arg 510	Gln 510	Gly 510
55	Arg 515	Phe 515	Leu 515	Trp 515	Glu 515	Thr 515	Tyr 520	Phe 520	Ser 520	Thr 520	Ala 520	Asp 525	Ser 525	Ile 525	Phe 525	Asn 525
60	Thr 530	Val 530	Leu 530	Ala 530	Met 530	Ile 535	Arg 535	Thr 535	Arg 535	Ile 535	Gln 535	Ile 540	Pro 540	Ala 540	Ala 540	Pro 540
65	Ile 545	Arg 545	Glu 545	Glu 545	Ala 545	Ala 550	Ala 550	Glu 550	Ile 550	Pro 555	His 555	Arg 555	Ser 555	Gly 555	Lys 555	Ala 560
70	Ala 570	Gly 570	Thr 570	Asp 570	Pro 565	Asn 565	Met 565	Ala 565	Asp 570	Asn 570	Gly 570	Asp 575	Leu 575	Asp 575	Leu 575	Gly 575
75	Pro 580	Val 580	Glu 580	Thr 580	Glu 580	Pro 580	Pro 580	Tyr 580	Ala 585	Ser 585	Pro 585	Arg 585	Tyr 590	Leu 590	Arg 590	Asn 590
80	Phe 595	Thr 595	Leu 595	Thr 595	Val 595	Thr 595	Asp 595	Phe 600	Tyr 600	Arg 600	Ser 600	Trp 600	Asn 605	Cys 605	Ala 605	Pro 605
85	Gly 610	Pro 610	Phe 610	His 610	Leu 610	Phe 615	Pro 615	His 615	Thr 615	Pro 615	Phe 615	Asp 620	Pro 620	Val 620	Leu 620	Pro 620
90	Ser 625	Glu 625	Ala 625	Lys 625	Phe 625	Leu 630	Gly 630	Ser 630	Gly 630	Thr 630	Gly 635	Phe 635	Arg 635	Pro 635	Ile 635	Gly 640
95	Gly 645	Gly 645	Ala 645	Gly 645	Gly 645	Ser 645	Gly 645	Lys 645	Glu 645	Phe 650	Gln 650	Ala 650	Ala 650	Leu 655	Gly 655	Gly 655
100	Asn 660	Val 660	Pro 660	Arg 660	Glu 660	Gln 660	Phe 660	Thr 665	Val 665	Val 665	Met 665	Leu 665	Thr 670	Tyr 670	Glu 670	Arg 670
105	Glu 675	Glu 675	Val 675	Leu 675	Met 675	Asn 675	Ser 675	Leu 680	Glu 680	Arg 680	Leu 680	Asn 685	Gly 685	Leu 685	Pro 685	Tyr 685
110	Leu 690	Asn 690	Lys 690	Val 690	Val 690	Val 695	Val 695	Trp 695	Asn 695	Ser 695	Pro 695	Lys 700	Leu 700	Pro 700	Ser 700	Glu 700


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Asp Leu Leu Trp Pro Asp Ile Gly Val Pro Ile Met Val Val Arg Thr
705              710              715              720

Glu Lys Asn Ser Leu Asn Asn Arg Phe Leu Pro Trp Asn Glu Ile Glu
5              725              730              735

Thr Glu Ala Ile Leu Ser Ile Asp Asp Ala His Leu Arg His Asp
              740              745              750

10Glu Ile Met Phe Gly Phe Arg Val Trp Arg Glu Ala Arg Asp Arg Ile
              755              760              765

Val Gly Phe Pro Gly Arg Tyr His Ala Trp Asp Ile Pro His Gln Ser
770              775              780

15Trp Leu Tyr Asn Ser Asn Tyr Ser Cys Glu Leu Ser Met Val Leu Thr
785              790              795              800

Gly Ala Ala Phe Phe His Lys Tyr Tyr Ala Tyr Leu Tyr Ser Tyr Val
20              805              810              815

Met Pro Gln Ala Ile Arg Asp Met Val Asp Glu Tyr Ile Asn Cys Glu
              820              825              830

25Asp Ile Ala Met Asn Phe Leu Val Ser His Ile Thr Arg Lys Pro Pro
835              840              845

Ile Lys Val Thr Ser Arg Trp Thr Phe Arg Cys Pro Gly Cys Pro Gln
850              855              860

30Ala Leu Ser His Asp Asp Ser His Phe His Glu Arg His Lys Cys Ile
865              870              875              880

Asn Phe Phe Val Lys Val Tyr Gly Tyr Met Pro Leu Leu Tyr Thr Gln
35              885              890              895

Phe Arg Val Asp Ser Val Leu Phe Lys Thr Arg Leu Pro His Asp Lys
900              905              910

40Thr Lys Cys Phe Lys Phe Ile
915

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(2) INFORMATION FOR SEQ ID NO:5:

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45 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 125 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

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50 (ii) MOLECULE TYPE: protein

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55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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Leu Cys Gly Glu Arg Glu Asp Arg Leu Glu Leu Leu Lys Leu Ser Thr
1              5              10              15

60 Phe Ala Leu Ile Ile Thr Pro Gly Asp Pro Arg Leu Val Ile Ser Ser
20              25              30

```

Gly Cys Ala Thr Arg Leu Phe Glu Ala Leu Glu Val Gly Ala Val Pro
 35 40 45
 Val Val Leu Gly Glu Gln Val Gln Leu Pro Tyr Gln Asp Met Leu Gln
 5 50 55 60
 Trp Asn Glu Ala Ala Leu Val Val Pro Lys Pro Arg Val Thr Glu Val
 65 70 75 80
 10 His Phe Leu Leu Arg Ser Leu Ser Asp Ser Asp Leu Leu Ala Met Arg
 85 90 95
 Arg Gln Gly Arg Phe Leu Trp Glu Thr Tyr Phe Pro Thr Ala Asp Ser
 100 105 110
 15 Ile Phe Asn Thr Val Leu Ala Met Ile Arg Thr Arg Ile
 115 120 125

(2) INFORMATION FOR SEQ ID NO:6:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 25 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
 Arg Cys His Lys His Gln Val Phe Asp Tyr Pro Gln Val Leu Gln Glu
 35 1 5 10 15
 Ala Thr Phe Cys Val Val Leu Arg Gly Ala Arg Leu Gly Gln Ala Val
 20 25 30
 40 Leu Ser Asp Val Leu Gln Ala Gly Cys Val Pro Val Val Ile Ala Asp
 35 40 45
 Ser Tyr Ile Leu Pro Phe Ser Glu Val Leu Asp Trp Lys Arg Ala Ser
 50 55 60
 45 Val Val Val Pro Glu Glu Lys Met Ser Asp Val Tyr Ser Ile Leu Gln
 65 70 75 80
 Ser Ile Pro Gln Arg Gln Ile Glu Glu Met Gln Arg Gln Ala Arg Trp
 50 85 90 95
 Phe Trp Glu Ala Tyr Phe Gln Ser Ile Lys Ala Ile Ala Leu Ala Thr
 100 105 110
 55 Leu Gln Ile Ile Asn Asp Arg Ile
 115 120

(2) INFORMATION FOR SEQ ID NO:7:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

036000 031001 103100 026000

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

10 Arg Cys Asp Arg Asp Asn Thr Glu Tyr Glu Lys Tyr Asp Tyr Arg Glu
 1 5 10 15
 Met Leu His Asn Ala Thr Phe Cys Leu Val Pro Arg Gly Arg Arg Leu
 20 25 30
 15 Gly Ser Phe Arg Phe Leu Glu Ala Leu Gln Ala Ala Cys Val Pro Val
 35 40 45
 Met Leu Ser Asn Gly Trp Glu Leu Pro Phe Ser Glu Val Ile Asn Trp
 50 55 60
 20 Asn Gln Ala Ala Val Ile Gly Asp Glu Arg Leu Leu Gln Ile Pro
 65 70 75 80
 25 Ser Thr Ile Arg Ser Ile His Gln Asp Lys Ile Leu Ala Leu Arg Gln
 85 90 95
 Gln Thr Gln Phe Leu Trp Glu Ala Tyr Phe Ser Ser Val Glu Lys Ile
 100 105 110
 30 Val Leu Thr Thr Leu Glu Ile Ile Gln Asp Arg Ile
 115 120

(2) INFORMATION FOR SEQ ID NO:8:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

50 Arg Cys Glu Gln Asp Pro Gly Pro Gly Gln Thr Gln Arg Gln Glu Thr
 1 5 10 15
 Leu Pro Asn Ala Thr Phe Cys Leu Ile Ser Gly His Arg Pro Glu Ala
 20 25 30
 55 Ala Ser Arg Phe Leu Gln Ala Leu Gln Ala Gly Cys Ile Pro Val Leu
 35 40 45
 Leu Ser Pro Arg Trp Glu Leu Pro Phe Ser Glu Val Ile Asp Trp Thr
 50 55 60
 60 Lys Ala Ala Ile Val Ala Asp Glu Arg Leu Pro Leu Gln Val Leu Ala
 65 70 75 80

Ala Leu Gln Glu Met Ser Pro Ala Arg Val Leu Ala Leu Arg Gln Gln
85 95

5 Thr Gln Phe Leu Trp Asp Ala Tyr Phe Ser Ser Val Glu Lys Val Ile
100 105 110

His Thr Thr Leu Glu Val Ile Gln Asp Arg Ile
115 120

10(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
15 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

25 Lys Cys Ser Gln Glu Asn Cys Ser Leu Glu Arg Arg Arg Gln Leu Ile
1 5 10 15

30 Gly Ser Ser Thr Phe Cys Phe Leu Leu Pro Ser Glu Met Phe Phe Gln
20 25 30

Asp Phe Leu Ser Ser Leu Gln Leu Gly Cys Ile Pro Ile Leu Leu Ser
35 40 45

35 Asn Ser Gln Leu Leu Pro Phe Gln Asp Leu Ile Asp Trp Arg Arg Ala
50 55 60

Thr Tyr Arg Leu Pro Leu Ala Arg Leu Pro Glu Ala His Phe Ile Val
65 70 75 80

40 Gln Ser Phe Glu Ile Ser Asp Ile Ile Glu Met Arg Arg Val Gly Arg
85 90 95

45 Leu Phe Tyr Glu Thr Tyr Leu Ala Asp Arg His Leu Leu Ala Arg Ser
100 105 110

Leu Leu Ala Ala Leu Arg Tyr Lys Leu
115 120

(2) INFORMATION FOR SEQ ID NO:10:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 262 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
55 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Val Pro Arg Glu Gln Phe Thr Val Val Met Leu Thr Tyr Glu Arg Glu
 1 5 10 15
 5 Glu Val Leu Met Asn Ser Leu Glu Arg Leu Asn Gly Leu Pro Tyr Leu
 20 25 30
 Asn Lys Val Val Val Val Trp Asn Ser Pro Lys Leu Pro Ser Glu Asp
 35 40 45
 10 Leu Leu Trp Pro Asp Ile Gly Val Pro Ile Met Val Val Arg Thr Glu
 50 55 60
 Lys Asn Ser Leu Asn Asn Arg Phe Leu Pro Trp Asn Glu Ile Glu Thr
 65 70 75 80
 15 Glu Ala Ile Leu Ser Ile Asp Asp Asp Ala His Leu Arg His Asp Glu
 85 90 95
 20 Ile Met Phe Gly Phe Arg Val Trp Arg Glu Ala Arg Asp Arg Ile Val
 100 105 110
 Gly Phe Pro Gly Arg Tyr His Ala Trp Asp Ile Pro His Gln Ser Trp
 115 120 125
 25 Leu Tyr Asn Ser Asn Tyr Ser Cys Glu Leu Ser Met Val Leu Thr Gly
 130 135 140
 Ala Ala Phe Phe His Lys Tyr Tyr Ala Tyr Leu Tyr Ser Tyr Val Met
 145 150 155 160
 30 Pro Gln Ala Ile Arg Asp Met Val Asp Glu Tyr Ile Asn Cys Glu Asp
 165 170 175
 35 Ile Ala Met Asn Phe Leu Val Ser His Ile Thr Arg Lys Pro Pro Ile
 180 185 190
 Lys Val Thr Ser Arg Trp Thr Phe Arg Cys Pro Gly Cys Pro Gln Ala
 195 200 205
 40 Leu Ser His Asp Asp Ser His Phe His Glu Arg His Lys Cys Ile Asn
 210 215 220
 Phe Phe Val Lys Val Tyr Gly Tyr Met Pro Leu Leu Tyr Thr Gln Phe
 225 230 235 240
 45 Arg Val Asp Ser Val Leu Phe Lys Thr Arg Leu Pro His Asp Lys Thr
 245 250 255
 50 Lys Cys Phe Lys Phe Ile
 260

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 269 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein

03809920.031601

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Lys Val Val Glu His Arg Ala Asp Pro Val Leu Tyr Lys Asp Asp Phe
245 250 255

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

5 Pro Pro Ser Lys Phe Thr Ala Val Ile His Ala Val Thr Pro Leu Val
1 5 10 15

Ser Gln Ser Gln Pro Val Leu Lys Leu Leu Val Ala Ala Ala Lys Ser
20 25 30

10 Gln Tyr Cys Ala Gln Ile Ile Val Leu Trp Asn Cys Asp Lys Pro Leu
35 40 45

15 Pro Ala Lys His Arg Trp Pro Ala Thr Ala Val Pro Val Val Val Ile
50 55 60

Glu Gly Glu Ser Lys Val Met Ser Ser Arg Phe Leu Pro Tyr Asp Asn
65 70 75 80

20 Ile Ile Thr Asp Ala Val Leu Ser Leu Asp Glu Asp Thr Val Leu Ser
85 90 95

Thr Thr Glu Val Asp Phe Ala Phe Thr Val Trp Gln Ser Phe Pro Glu
100 105 110

25 Arg Ile Val Gly Tyr Pro Ala Arg Ser His Phe Trp Asp Asn Ser Lys
115 120 125

Glu Arg Trp Gly Tyr Thr Ser Lys Trp Thr Asn Asp Tyr Ser Met Val
130 135 140

30 Leu Thr Gly Ala Ala Ile Tyr His Lys Tyr Tyr His Tyr Leu Tyr Ser
145 150 155 160

35 His Tyr Leu Pro Ala Ser Leu Lys Asn Met Val Asp Gln Leu Ala Asn
165 170 175

Cys Glu Asp Ile Leu Met Asn Phe Leu Val Ser Ala Val Thr Lys Leu
180 185 190

40 Pro Pro Ile Lys Val Thr Gln Lys Lys Gln Tyr Lys Glu Thr Met Met
195 200 205

Gly Gln Thr Ser Arg Ala Ser Arg Trp Ala Asp Pro Asp His Phe Ala
210 215 220

45 Gln Arg Gln Ser Cys Met Asn Thr Phe Ala Ser Trp Phe Gly Tyr Met
225 230 235 240

50 Pro Leu Ile His Ser Gln Met Arg Leu Asp Pro Val Leu Lys Asp Gln
245 250 255

Val Ser Ile Leu Arg Lys Lys Tyr Arg Asp Ile Glu Arg Leu
260 265 270

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 262 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

10 Pro Glu Gly Arg Phe Ser Ala Leu Ile Trp Val Gly Pro Pro Gly Gln
1 5 10 15

Pro Pro Leu Lys Leu Ile Gln Ala Val Ala Gly Ser Gln His Cys Ala
20 25 30

15 Gln Ile Leu Val Leu Trp Ser Asn Glu Arg Pro Leu Pro Ser Arg Trp
35 40 45

Pro Glu Thr Ala Val Pro Leu Thr Val Ile Asp Gly His Arg Lys Val
50 55 60

20 Ser Asp Arg Phe Tyr Pro Tyr Ser Thr Ile Arg Thr Asp Ala Ile Leu
65 70 75 80

Ser Leu Asp Ala Arg Ser Ser Leu Ser Thr Ser Glu Val Asp Phe Ala
85 90 95

25 Phe Leu Val Trp Gln Ser Phe Pro Glu Arg Met Val Gly Phe Leu Thr
100 105 110

30 Ser Ser His Phe Trp Asp Glu Ala His Gly Gly Trp Gly Tyr Thr Ala
115 120 125

Glu Arg Thr Asn Glu Phe Ser Met Val Leu Thr Thr Ala Ala Phe Tyr
130 135 140

35 His Arg Tyr Tyr His Thr Leu Phe Thr His Ser Leu Pro Lys Ala Leu
145 150 155 160

Arg Thr Leu Ala Asp Glu Ala Pro Thr Cys Val Asp Val Leu Met Asn
165 170 175

40 Phe Ile Val Ala Ala Val Thr Lys Leu Pro Pro Ile Lys Val Pro Tyr
180 185 190

45 Gly Lys Gln Arg Gln Glu Ala Ala Pro Leu Ala Pro Gly Gly Pro Gly
195 200 205

Pro Arg Pro Lys Pro Pro Ala Pro Ala Pro Asp Cys Ile Asn Gln Ile
210 215 220

50 Ala Ala Ala Phe Gly His Met Pro Leu Leu Ser Ser Arg Leu Arg Leu
225 230 235 240

Asp Pro Val Leu Phe Lys Asp Pro Val Ser Val Gln Arg Lys Lys Tyr
245 250 255

55 Arg Ser Leu Glu Lys Pro
260

(2) INFORMATION FOR SEQ ID NO:14:

60

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 270 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

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5
10  Ser Thr Met Asp Ser Phe Thr Leu Ile Met Gln Thr Tyr Asn Arg Thr
    1          5          10          15
15  Asp Leu Leu Leu Lys Leu Leu Asn His Tyr Gln Ala Val Pro Asn Leu
    20          25          30
20  His Lys Val Ile Val Val Trp Asn Ile Gly Glu Lys Ala Pro Asp
    35          40          45
25  Glu Leu Trp Asn Ser Leu Gly Pro His Pro Ile Pro Val Ile Phe Lys
    50          55          60
    Gln Gln Thr Ala Asn Arg Met Arg Asn Arg Leu Gln Val Phe Pro Glu
    65          70          75          80
25  Leu Glu Thr Asn Ala Val Leu Met Val Asp Asp Thr Leu Ile Ser
    85          90          95
30  Thr Pro Asp Leu Val Phe Ala Phe Ser Val Trp Gln Gln Phe Pro Asp
    100          105          110
    Gln Ile Val Gly Phe Val Pro Arg Lys His Val Ser Thr Ser Ser Gly
    115          120          125
35  Ile Tyr Ser Tyr Gly Ser Phe Glu Met Gln Ala Pro Gly Ser Gly Asn
    130          135          140
    Gly Asp Gln Tyr Ser Met Val Leu Ile Gly Ala Ser Phe Phe Asn Ser
    145          150          155          160
40  Lys Tyr Leu Glu Leu Phe Gln Arg Gln Pro Ala Ala Val His Ala Leu
    165          170          175
    Ile Asp Asp Thr Gln Asn Cys Asp Asp Ile Ala Met Asn Phe Ile Ile
    180          185          190
45  Ala Lys His Ile Gly Lys Thr Ser Gly Ile Phe Val Lys Pro Val Asn
    195          200          205
50  Met Asp Asn Leu Glu Lys Glu Thr Asn Ser Gly Tyr Ser Gly Met Trp
    210          215          220
    His Arg Ala Glu His Ala Leu Gln Arg Ser Tyr Cys Ile Asn Lys Leu
    225          230          235          240
55  Val Asn Ile Tyr Asp Ser Met Pro Leu Arg Tyr Ser Asn Ile Met Ile
    245          250          255
60  Ser Gln Phe Gly Phe Pro Tyr Ala Asn Tyr Lys Arg Lys Ile
    260          265          270

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(2) INFORMATION FOR SEQ ID NO:15:

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Lys Tyr Val

(2) INFORMATION FOR SEQ ID NO:16:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTATGGCGAG TGACCCGACG TG

22

20 (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: DNA (genomic)
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

35 TTGCTAAAGT GAAGGAAGTT GG

22

(2) INFORMATION FOR SEQ ID NO:18:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 45 (ii) MOLECULE TYPE: DNA (genomic)

- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACCCGACGTG ATCTGG

16

(2) INFORMATION FOR SEQ ID NO:19:

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 60 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

5AAGAGCTCCT GCAGCTGG

18

(2) INFORMATION FOR SEQ ID NO:20:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTCTCGTTGC CCTCTCAC

18

(2) INFORMATION FOR SEQ ID NO:21:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 30 (ii) MOLECULE TYPE: DNA (genomic)

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATCATCAATC TGTCACG

17

40 (2) INFORMATION FOR SEQ ID NO:22:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: DNA (genomic)

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACTACGATGA CCGGATC

17

(2) INFORMATION FOR SEQ ID NO:23:

- 60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

10TTCCTACCA GGACATGC

18

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AACATGGCTG ACAACG

16

(2) INFORMATION FOR SEQ ID NO:25:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA (genomic)

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TATTGGTGGT GGAGCTGG

18

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(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

60

AATCCAGCCA TGGTCTCCTT GG

22

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGTCGATGCC ATTATTACCA GC

22

15

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TTCCTTCCTC ATCACAG

17

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(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGGTCTGTGT ATGCACTTGT G

21

50 (2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGTCGATGCC ATTATTACCA GC

22

(2) INFORMATION FOR SEQ ID NO:31:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: DNA (genomic)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTCAAGGGTG TGGAGAG

17

20 (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: DNA (genomic)

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

35 TTGGCTGAAA GCCAACACCC TG

22

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: DNA (genomic)

45 (ii) MOLECULE TYPE: DNA (genomic)

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AACATGCACG CATCCACAGC

20

(2) INFORMATION FOR SEQ ID NO:34:

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 60 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

5TTGTAACACA GCATGTGG

18

(2) INFORMATION FOR SEQ ID NO:35:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGTTCTGTCA GTATTAGCTG GG

22

(2) INFORMATION FOR SEQ ID NO:36:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

40 TTCCTCCCTC TGCTCATCCT C

21

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

55 TTCCCACTCT GTCTCTC

17